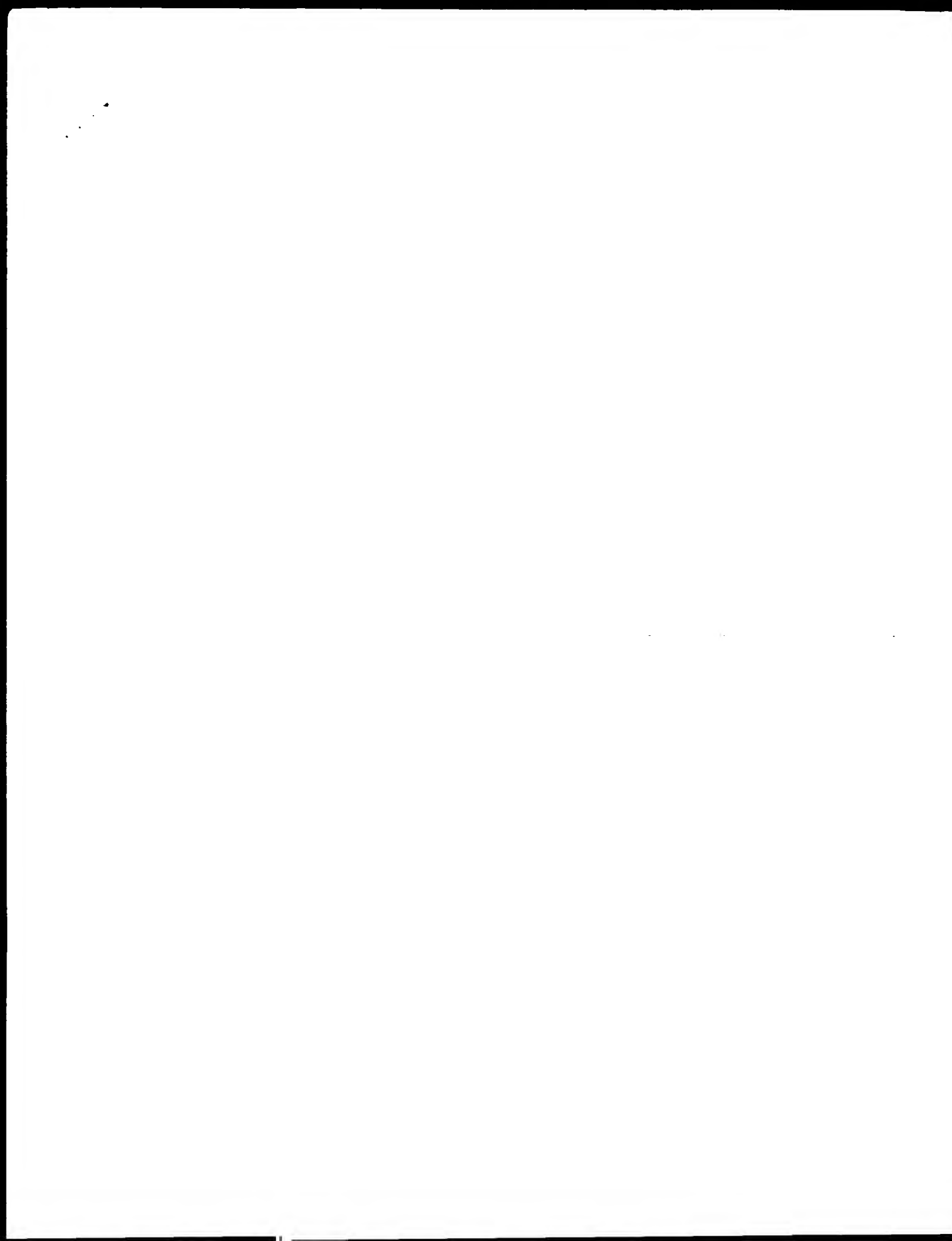


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Mon Mar 11 17:09:32 2002

us-09-503-387-3.rpt

Page 7



GenDate version 4.5
Copyright (c) 1995 - 2000, Compugen Ltd.

AM Protein - Protein search using SW model

Run on: March 11, 2002, 12:01:05.1 Search time for 1 sequence
(with 2000 iterations)
42.64 Megabits/sec of bytes/sec

Full Seq: 05-09-503-387-3_134_180.rsp
Footprint score: 269
Sequence: 1 (0) K1214_HUMAN.....

Scoring table: BLOSUM62

Gapop: 10.0, Gapext: 0.5

Searched: 106059 seqs, 6664427 residues

Total number of hits satisfying chosen parameters: 1 hit

Minimum E-value for hit: 0

Maximum JPS Seq length: 200000000

Fast Forward: Maximum Match: 70

Maximum Match: 70

Listed first 45 matches

Database: 1 SWISSProt_391*

Prod. No. is the number of results provided by the search. It is a score greater than or equal to the score of the best hit and printed and is divided by analysis of the total score divided by 1.

SUMMARY

Result No.	Score	Match Length	ID	Accession	Length	Score	Score
1	53	41.7	1	K214_HUMAN	271	100	100
2	49	41.2	1	K121_HUMAN	271	100	100
3	49	40.7	1	K121_HUMAN	271	100	100
4	49	40.7	1	K121_HUMAN	271	100	100
5	49	40.7	1	K121_HUMAN	271	100	100
6	49	40.7	1	K121_HUMAN	271	100	100
7	49	40.7	1	K121_HUMAN	271	100	100
8	49	40.7	1	K121_HUMAN	271	100	100
9	49	40.7	1	K121_HUMAN	271	100	100
10	49	40.7	1	K121_HUMAN	271	100	100
11	49	40.7	1	K121_HUMAN	271	100	100
12	49	40.7	1	K121_HUMAN	271	100	100
13	49	40.7	1	K121_HUMAN	271	100	100
14	49	40.7	1	K121_HUMAN	271	100	100
15	49	40.7	1	K121_HUMAN	271	100	100
16	49	40.7	1	K121_HUMAN	271	100	100
17	49	40.7	1	K121_HUMAN	271	100	100
18	49	40.7	1	K121_HUMAN	271	100	100
19	49	40.7	1	K121_HUMAN	271	100	100
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21	49	40.7	1	K121_HUMAN	271	100	100
22	49	40.7	1	K121_HUMAN	271	100	100
23	49	40.7	1	K121_HUMAN	271	100	100
24	49	40.7	1	K121_HUMAN	271	100	100
25	49	40.7	1	K121_HUMAN	271	100	100
26	49	40.7	1	K121_HUMAN	271	100	100
27	49	40.7	1	K121_HUMAN	271	100	100
28	49	40.7	1	K121_HUMAN	271	100	100
29	49	40.7	1	K121_HUMAN	271	100	100
30	49	40.7	1	K121_HUMAN	271	100	100
31	49	40.7	1	K121_HUMAN	271	100	100
32	49	40.7	1	K121_HUMAN	271	100	100
33	49	40.7	1	K121_HUMAN	271	100	100

ALIGNMENTS

Result ID	Score	Match Length	ID	Accession	Length	Score	Score
1	53	41.7	1	K214_HUMAN	271	100	100
2	49	41.2	1	K121_HUMAN	271	100	100
3	49	40.7	1	K121_HUMAN	271	100	100
4	49	40.7	1	K121_HUMAN	271	100	100
5	49	40.7	1	K121_HUMAN	271	100	100
6	49	40.7	1	K121_HUMAN	271	100	100
7	49	40.7	1	K121_HUMAN	271	100	100
8	49	40.7	1	K121_HUMAN	271	100	100
9	49	40.7	1	K121_HUMAN	271	100	100
10	49	40.7	1	K121_HUMAN	271	100	100
11	49	40.7	1	K121_HUMAN	271	100	100
12	49	40.7	1	K121_HUMAN	271	100	100
13	49	40.7	1	K121_HUMAN	271	100	100
14	49	40.7	1	K121_HUMAN	271	100	100
15	49	40.7	1	K121_HUMAN	271	100	100
16	49	40.7	1	K121_HUMAN	271	100	100
17	49	40.7	1	K121_HUMAN	271	100	100
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21	49	40.7	1	K121_HUMAN	271	100	100
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25	49	40.7	1	K121_HUMAN	271	100	100
26	49	40.7	1	K121_HUMAN	271	100	100
27	49	40.7	1	K121_HUMAN	271	100	100
28	49	40.7	1	K121_HUMAN	271	100	100
29	49	40.7	1	K121_HUMAN	271	100	100
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31	49	40.7	1	K121_HUMAN	271	100	100
32	49	40.7	1	K121_HUMAN	271	100	100
33	49	40.7	1	K121_HUMAN	271	100	100

[illegible][illegible]

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us-09-503-387-3_copy_134_180.rsp

Page 12

Mon Mar 11 17:09:29 2002

us-09-503-387-3.rai

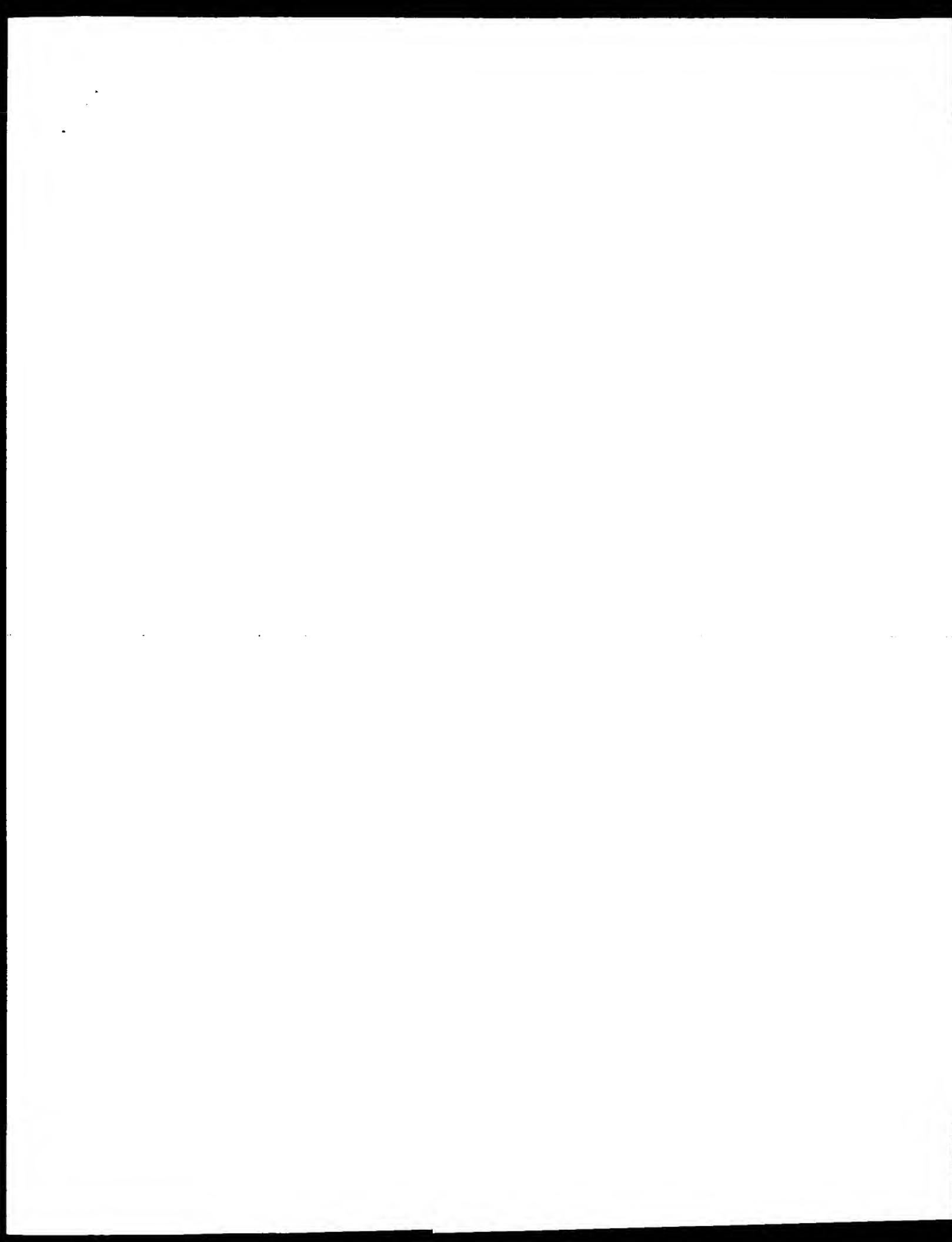
Page 8

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10 24 VERIFIED/RECEIVED VAP 266

Search completed: March 11, 2002, 16:44:45
Job Time: 419 sec



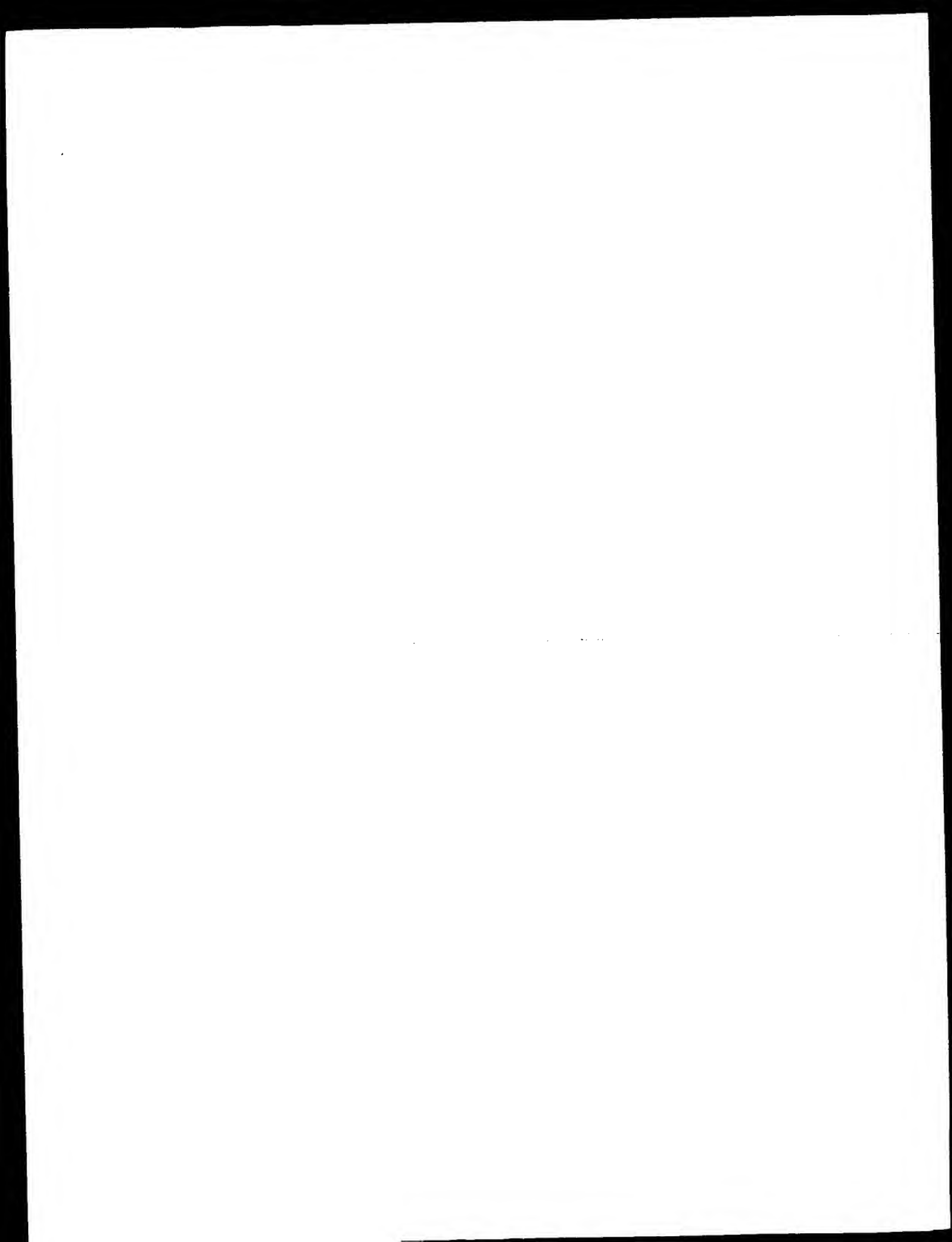
Best local similarity 46.1%; Prod. No. 9,500 of 100 matches 77; Conservat. 45; Recomb. 100; 100



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Page 11



SMAR1: SM00410; 61.1Kb; 1
 K6: 100% (1000/1000) IDENTITY: 100% (1000/1000)
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 S0: 100% (1000/1000) IDENTITY: 100% (1000/1000)

Query Match: 41.78% Score: 68.5; 10.1; 10.0
 Best Local Similarity: 48.08% Prod. No. 0.29
 Matches: 19; Conserved: 19; Mismatches: 19; Gaps: 1

1. 100% (1000/1000) IDENTITY: 100% (1000/1000)
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RESULTS 9
 075024 PRELIMINARY: FRT: 50.0 AA
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Query Match: 41.24% Score: 67.5; 10.1; 10.0
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Yamashita Y., Fukuda Y., Tsuji A., Nakamura A., Matsuda Y.,
 Nishikawa Y., Ohgawa Y., Ohmura H., Oono M., Takai T.,
 J. Biol. Chem. 273: 12510-12516 (1998)

Query Match: 41.78% Score: 68.5; 10.1; 10.0
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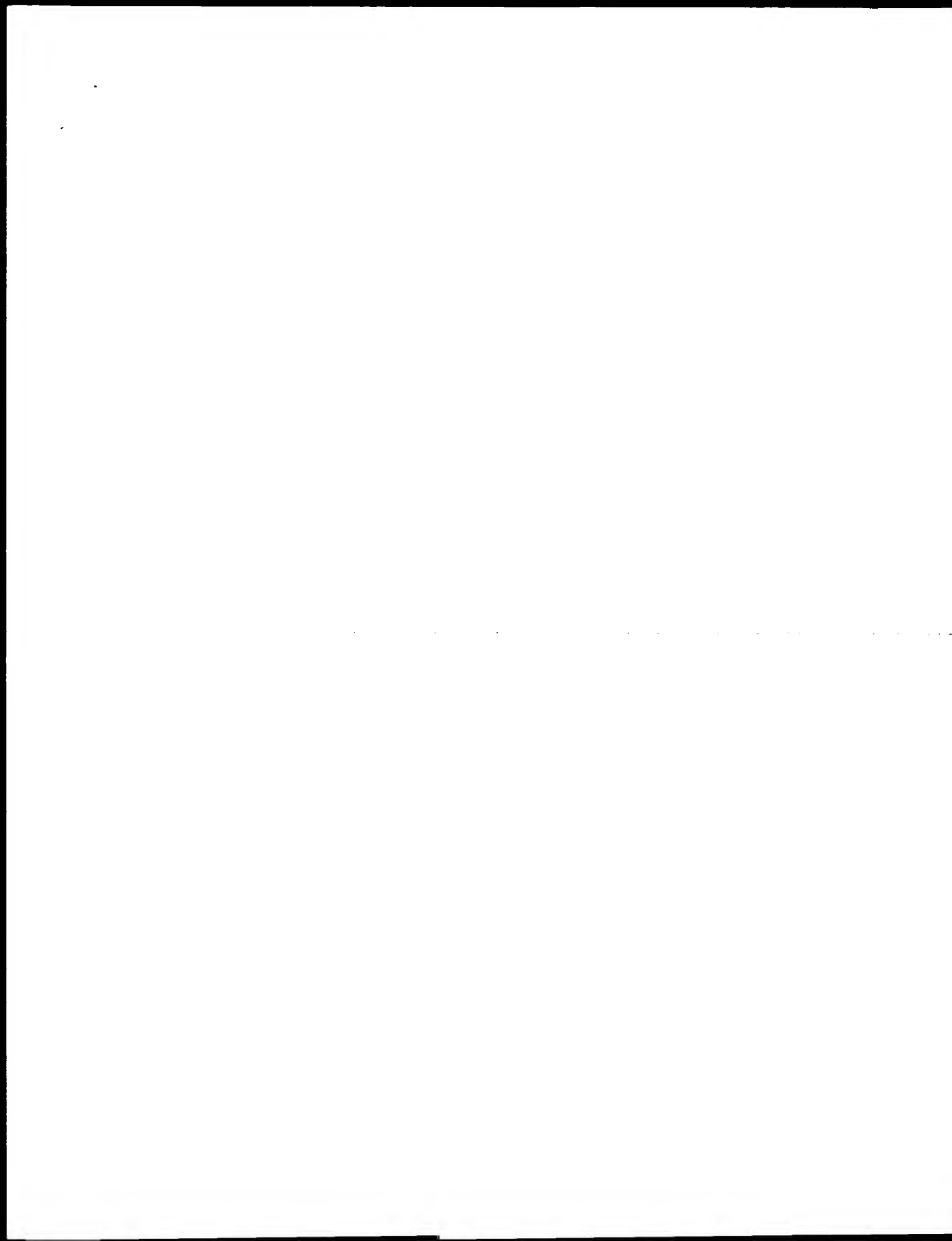
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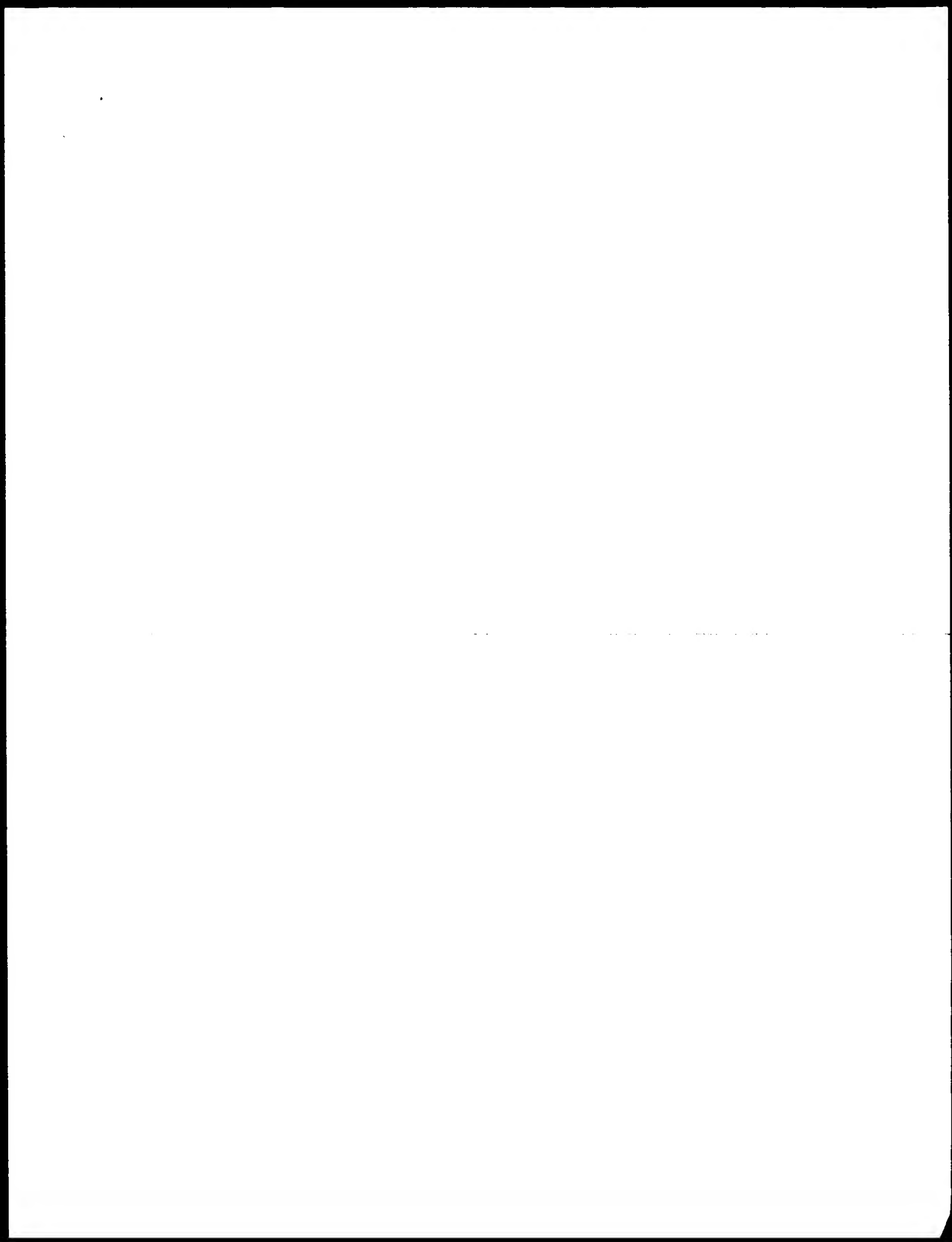
RESULTS 11
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Query Match: 41.24% Score: 67.5; 10.1; 10.0
 Best Local Similarity: 48.08% Prod. No. 0.29
 Matches: 19; Conserved: 19; Mismatches: 19; Gaps: 1

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106 W01: 2001 08067709.
 XX
 11 New genes encoding human platelet expressed collagen receptors,
 12 glycoprotein VI, and its modulators, useful for prevention, treatment
 13 and diagnosis of hemorrhagic disorders, thrombotic diseases and
 14 immunological disorders.
 15
 16 [Enclosure Page 203: 227pp: English].
 17
 18 The present sequence is given in a specification relating to an isolated
 19 nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 20 glycoprotein VI (GPVI), also called IAM2/268. The GPVI polypeptide has
 21 and polypeptides and their modulators, e.g., and those covalently
 22 ribozymes and antibodies, are useful for preventing, treating and
 23 diagnosing disorders associated with aberrant expression or activity of
 24 GPVI. These disorders include bleeding disorders
 25 (e.g., thrombocytopenia), blood vessel injury, thrombotic disorders
 26 (e.g., thrombotic occlusion of the coronary arteries), hemorrhagic
 27 disorders, coronary artery and cerebral artery diseases (e.g., stroke and
 28 ischemia), cardiovascular diseases (e.g., atherosclerosis and myocardial
 29 infarction), immunological diseases (e.g., platelet disorder) and
 30 embryonic liver disorders. Preferably they are used to prevent acute
 31 cardiac ischemia following angioplasty and myocardial infarction,
 32 especially of the colon and liver.
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 34 Sequence: 41 AA.
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Matches	24	Conservative	10	Mismatches	12	Indels	0	Ref	52
CC	11	11	11	11	11	11	11	11	11
UU	11	11	11	11	11	11	11	11	11
UU	11	11	11	11	11	11	11	11	11

Search completed: March 11, 2002, 17:02:18
 Job Time: 2012 sec

US-09-445-468-9

Query Match: 100.0% Score: 2687 100.4% Length: 47
 Host Local Similarity: 100.0% Prod. No. 1 to 40
 Matches: 47. Character set: 03. Mismatched: 00. Tuples: 00

US-09-445-468-9
 1 100.0% 2687 100.4% 47
 114 100.0% 2687 100.4% 47

RESULT 4

US-09-445-468-9
 Sequence: 5. Application US/09-445-468
 Patent No. 6,245,627
 GENERAL INFORMATION:
 APPLICANT: Bushfield, S.
 APPLICANT: Villalobos, J.
 APPLICANT: Jandrot-Perrus, M.
 APPLICANT: Villalobos, J.
 TITLE OF INVENTION: GLYCOPEPTIN VI AND USES THEREOF
 FILE REFERENCE: 7853-147
 CURRENT APPLICATION NUMBER: US/09-445-468
 CURRENT FILING DATE: 1999-06-30
 NUMBER OF SEQ. ID NOS: 24
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ. ID No: 5
 LENGTH: 47
 TYPE: PPT
 ORGANISM: Homo sapiens
 US-09-445-468-9

Query Match: 100.0% Score: 2687 100.4% Length: 47
 Host Local Similarity: 100.0% Prod. No. 1 to 40
 Matches: 47. Character set: 03. Mismatched: 00. Tuples: 00

US-09-445-468-9
 1 100.0% 2687 100.4% 47
 114 100.0% 2687 100.4% 47

RESULT 4

US-09-445-468-9
 Sequence: 5. Application US/09-445-468
 Patent No. 6,245,627
 GENERAL INFORMATION:
 APPLICANT: Bushfield, S.
 APPLICANT: Villalobos, J.
 APPLICANT: Jandrot-Perrus, M.
 APPLICANT: Villalobos, J.
 TITLE OF INVENTION: GLYCOPEPTIN VI AND USES THEREOF
 FILE REFERENCE: 7853-147
 CURRENT APPLICATION NUMBER: US/09-445-468
 CURRENT FILING DATE: 1999-06-30
 NUMBER OF SEQ. ID NOS: 24
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ. ID No: 5
 LENGTH: 47
 TYPE: PPT
 ORGANISM: Homo sapiens
 US-09-445-468-9

Query Match: 100.0% Score: 2687 100.4% Length: 47
 Host Local Similarity: 100.0% Prod. No. 1 to 40
 Matches: 47. Character set: 03. Mismatched: 00. Tuples: 00

US-09-445-468-9
 1 100.0% 2687 100.4% 47
 114 100.0% 2687 100.4% 47

RESULT 5

US-09-445-468-24
 Sequence: 24. Application US/09-445-468
 Patent No. 6,245,627
 GENERAL INFORMATION:
 APPLICANT: Bushfield, S.
 APPLICANT: Villalobos, J.
 APPLICANT: Jandrot-Perrus, M.
 APPLICANT: Villalobos, J.
 TITLE OF INVENTION: GLYCOPEPTIN VI AND USES THEREOF
 FILE REFERENCE: 7853-147
 CURRENT APPLICATION NUMBER: US/09-445-468
 CURRENT FILING DATE: 1999-06-30
 NUMBER OF SEQ. ID NOS: 24
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ. ID No: 24
 LENGTH: 47
 TYPE: PPT
 ORGANISM: Mus musculus
 US-09-445-468-24

Query Match: 82.1% Score: 2202 100.4% Length: 47
 Host Local Similarity: 78.7% Prod. No. 1 to 40
 Matches: 47. Character set: 47. Mismatched: 00. Tuples: 00

US-09-445-468-24
 1 82.1% 2202 100.4% 47
 114 78.7% 2202 100.4% 47

RESULT 6

US-09-445-468-19
 Sequence: 19. Application US/09-445-468
 Patent No. 6,245,627
 GENERAL INFORMATION:
 APPLICANT: Bushfield, S.
 APPLICANT: Villalobos, J.
 APPLICANT: Jandrot-Perrus, M.
 APPLICANT: Villalobos, J.
 TITLE OF INVENTION: GLYCOPEPTIN VI AND USES THEREOF
 FILE REFERENCE: 7853-147
 CURRENT APPLICATION NUMBER: US/09-445-468
 CURRENT FILING DATE: 1999-06-30
 NUMBER OF SEQ. ID NOS: 24
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ. ID No: 19
 LENGTH: 267
 TYPE: PPT
 ORGANISM: Mus musculus
 US-09-445-468-19

Query Match: 62.1% Score: 2202 100.4% Length: 47
 Host Local Similarity: 78.7% Prod. No. 1 to 40
 Matches: 47. Character set: 47. Mismatched: 00. Tuples: 00

US-09-445-468-19
 1 62.1% 2202 100.4% 47
 114 78.7% 2202 100.4% 47

RESULT 7

US-09-445-468-18
 Sequence: 18. Application US/09-445-468
 Patent No. 6,245,627
 GENERAL INFORMATION:
 APPLICANT: Bushfield, S.
 APPLICANT: Villalobos, J.
 APPLICANT: Jandrot-Perrus, M.
 APPLICANT: Villalobos, J.
 TITLE OF INVENTION: GLYCOPEPTIN VI AND USES THEREOF
 FILE REFERENCE: 7853-147
 CURRENT APPLICATION NUMBER: US/09-445-468
 CURRENT FILING DATE: 1999-06-30
 NUMBER OF SEQ. ID NOS: 24
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ. ID No: 18
 LENGTH: 267
 TYPE: PPT
 ORGANISM: Mus musculus
 US-09-445-468-18

Query Match: 62.1% Score: 2202 100.4% Length: 47
 Host Local Similarity: 78.7% Prod. No. 1 to 40
 Matches: 47. Character set: 47. Mismatched: 00. Tuples: 00

TITLE OF INVENTION: Isolated Mammalian B-cells
 NUMBER OF SEQUENCES: 22
 ADDRESS: 1000 Research Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patented in Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 01-01-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 21-MARCH-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 16-03-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 06-DEC-1996
 ALTERNATIVE INFORMATION:
 NAME: John, John P.
 REFERENCE NUMBER: 44,000
 REFERENCE NUMBER: 44,000
 TELEPHONE: (650)852-1204
 TELEFAX: (650)496-1204
 INFORMATION: 09/000000
 SEQUENCE CHARACTERISTICS:
 LENGTH: 651 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US 09 985 950-22

Query Match: 46.08% Score 96.5% DB: 47
 Host Local Similarity: 42.08% Prod. No. 1.0.05
 Matched: 22 Sequences 100 Matches 120 in 47
 US 09 985 950-22
 RESULT: 12
 US 09 985 950-22
 Sequence 10, Application US/090950
 GENERAL INFORMATION:
 APPLICANT: Alameda, Jesse Jan
 TITLE OF INVENTION: Isolated Mammalian B-cells
 NUMBER OF SEQUENCES: 22
 ADDRESS: 1000 Research Avenue
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patented in Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 01-01-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 21-MARCH-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 16-03-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 06-DEC-1996
 ALTERNATIVE INFORMATION:
 NAME: John, John P.

Query Match: 46.08% Score 96.5% DB: 47
 Host Local Similarity: 42.08% Prod. No. 1.0.05
 Matched: 22 Sequences 100 Matches 120 in 47
 US 09 985 950-22
 RESULT: 12
 US 09 985 950-22
 Sequence 10, Application US/090950
 GENERAL INFORMATION:
 APPLICANT: Alameda, Jesse Jan
 TITLE OF INVENTION: Isolated Mammalian B-cells
 NUMBER OF SEQUENCES: 22
 ADDRESS: 1000 Research Avenue
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patented in Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 01-01-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 21-MARCH-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 16-03-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 06-DEC-1996
 ALTERNATIVE INFORMATION:
 NAME: John, John P.

Query Match: 46.08% Score 96.5% DB: 47
 Host Local Similarity: 42.08% Prod. No. 1.0.05
 Matched: 22 Sequences 100 Matches 120 in 47
 US 09 985 950-22
 RESULT: 12
 US 09 985 950-22
 Sequence 10, Application US/090950
 GENERAL INFORMATION:
 APPLICANT: Alameda, Jesse Jan
 TITLE OF INVENTION: Isolated Mammalian B-cells
 NUMBER OF SEQUENCES: 22
 ADDRESS: 1000 Research Avenue
 STREET: 901 California Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patented in Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 01-01-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 21-MARCH-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 16-03-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/000000
 FILING DATE: 06-DEC-1996
 ALTERNATIVE INFORMATION:
 NAME: John, John P.

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Page 6

GenCore version 1.5
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001 Protocol: Protein search, using SW model

Run on: March 11, 2002, 12:00:06, Search time: 1.1 sec, 0.06 sec

(with an additional 0.06 sec)

Hit list: 08 09 503 387 3 copy_21_269

Percent score: 100

Sequence: 1 GSNAPRPSVALSLVPL.....SRKPSLAVAGLYR N 419

Scoring table:

Gap: 10.0, expect 0.5

Search: 100000 seqs, 4664827 total

Minimum job seq length: 6

Maximum job seq length: 2000000

Post processing: Maximum hit: 100

Database: SwissProt_000000

Note: No. is the number of results provided to the user. Score above that or equal to the score of the top hit is included, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	Hit	Accession
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2	42.2	24.7	291	1	KSL_HUMAN	U04344
3	42.0	24.6	444	1	KSL_HUMAN	U04344
4	41.7	24.5	291	1	KSL_HUMAN	U04344
5	41.4	24.1	291	1	KSL_HUMAN	U04344
6	41.4	24.1	291	1	KSL_HUMAN	U04344
7	41.4	24.1	291	1	KSL_HUMAN	U04344
8	41.4	24.1	291	1	KSL_HUMAN	U04344
9	40.5	23.6	484	1	KSL_HUMAN	U04344
10	39.2	23.2	445	1	KSL_HUMAN	U04344
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ALIGNMENTS

Result	Query	Hit	Score	Accession	Comments
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2	KSL_HUMAN	KSL_HUMAN	42.2	U04344	
3	KSL_HUMAN	KSL_HUMAN	42.0	U04344	
4	KSL_HUMAN	KSL_HUMAN	41.7	U04344	
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7	KSL_HUMAN	KSL_HUMAN	41.4	U04344	
8	KSL_HUMAN	KSL_HUMAN	41.4	U04344	
9	KSL_HUMAN	KSL_HUMAN	40.5	U04344	
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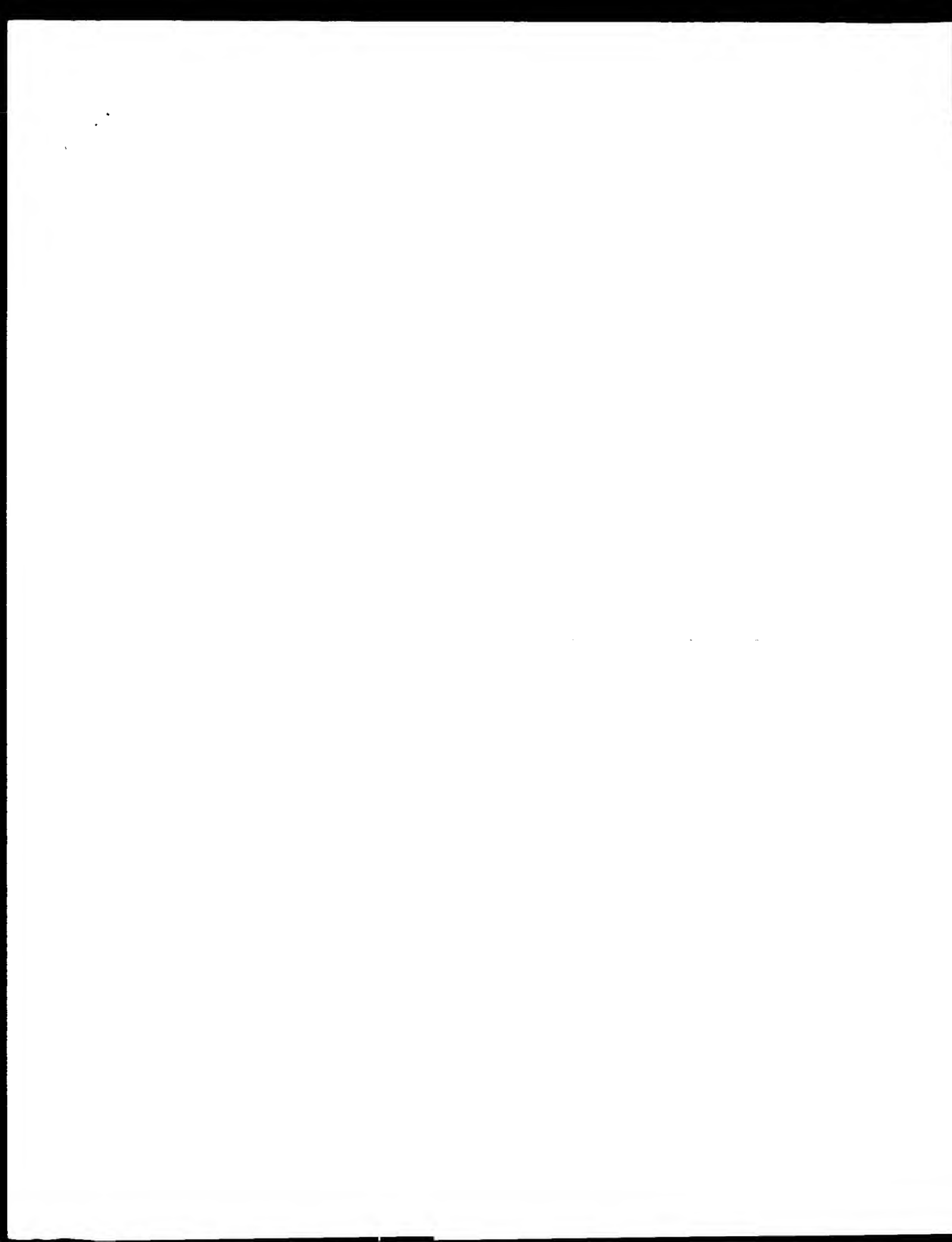
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Mon Mar 11 17:09:44 2002

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Page 13

Search completed: March 11, 2002, 17:00:47
Job time: 006 sec



Database Version: 1.5
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Run on: March 11, 2002, 16:44:45.3 Search time: 0:01:05.0

(with all matches)

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Page 14

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Page 8

Search completed: March 11, 2002, 17:09:11
Indexing: 104, 800

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THE PROBLEM OF THE SECTORIAL UNIONS

Kullback-Leibler divergence

$$D_{KL}(P \parallel Q) = \sum_i P(i) \log \frac{P(i)}{Q(i)}$$

Introduction

[illegible]
$$S_{\text{eff}} = \int d^4x \sqrt{-g} \left[\frac{1}{2} R - \frac{1}{2} (\partial_\mu \phi)^2 - V(\phi) \right]$$

Sector Labels: H1, S1M1Z

Submitted: 11/15/2005

[illegible][illegible]

Maximum length: 2000000

Post-Processual Material, 114

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Result and conclusion

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US 07 971 092 2
Sequence 2, Application US/07/01092
Patent No. 5429687

GENERAL INFORMATION:
APPLICANT: POLICE, CLAUDE R
TITLE OF INVENTION: Method for Reception
NUMBER OF SHEETS: 2
CORRESPONDENCE ADDRESS:
ADDRESSMENT: IMMEDIATE
STREET: 51 UNIVERSITY
CITY: SCHAFF
STATE: WA
COUNTRY: USA
ZIP: 98104

COMPUTER GENERATED:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: PLOTTER PROGRAM #1.0, Version #1.0,
CURRENT APPLICATION DATA
APPLICATION NUMBER: 05/207,201 002
FILING DATE: 19921104
CLASSIFICATION: F35

ATTORNEY/AGENT INFORMATION:
NAME: FORTIN, GUY-LEON
REGISTRATION NUMBER: 44694
REFERENCE/AGENT: 999999999999
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE INFORMATION:
LENGTH: 287 amino acids
TYPE: AMINO ACIDS
IMPORTANCE: High

MULTIPLE TYPE: protein
US 07 971 092 2

[illegible]

FILE IN DATE: 195 JUN 1996
: SEQ TO NO: 2:
: JENNYH: 287
: 198642-2

[illegible]

RESUME 1 to
 US 08 985-760 22
 SECTION 22: Application US/08095760
 Patent No. 6140076
 GENERAL INFORMATION:
 APPLICANT: Academia, Crosss Ltd
 TITLE OF INVENTION: Isolated Murine Anti Murine CD33 Antibody
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 Academia, 2000 Research Institute
 STREET 901 California Avenue
 CITY Palo Alto
 STATE California
 COUNTRY USA
 ZIP: 94304 1104
 PUBLICATION DATE: 1998
 MEDICAL TYPE: Therapy drug
 OPERATING SYSTEM: Windows 95
 SOFTWARE: Patent to Invention #1.0, Version #1.40
 PUBLISHED APPLICATION DATA:
 PUBLICATION: 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22
 FILING DATE: 05 DEC 1997
 PRIORITY DATE: 05 DEC 1996
 PRIORITY APPLICATION: 435
 PUBLICATION DATA:
 APPLICATION NUMBER: US 80/041,273
 FILING DATE: 21 MARCH 1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 86/00434, 181
 FILING DATE: 16 DEC 1996
 PUBLICATION DATA:
 APPLICATION NUMBER: US 86/012,252
 FILING DATE: 06 DEC 1996
 APPLICATION: Application:
 NAME: Third, Edgar P.
 REGISTRATION NUMBER: 44,000
 REFERENCE TO OTHER DOCUMENTS:
 PUBLICATION: Application:

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Match	122	Consecutive	44	Mismatch
			135	Induct
			44	Match

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115.08 "307-3.0" 14

: **SYNOPSIS:** A child, aged 22/30/1972
 : National No. 614076
 : **GENERAL INFORMATION:**
 : **APPLICANT:** Adnan, GOSSE, Ed
 : **TITLE OF INVENTION:** Improved Method of

MOLECULAR WEIGHT: 17,000
 CRYSTALLINITY: 0.00-0.14

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[illegible]

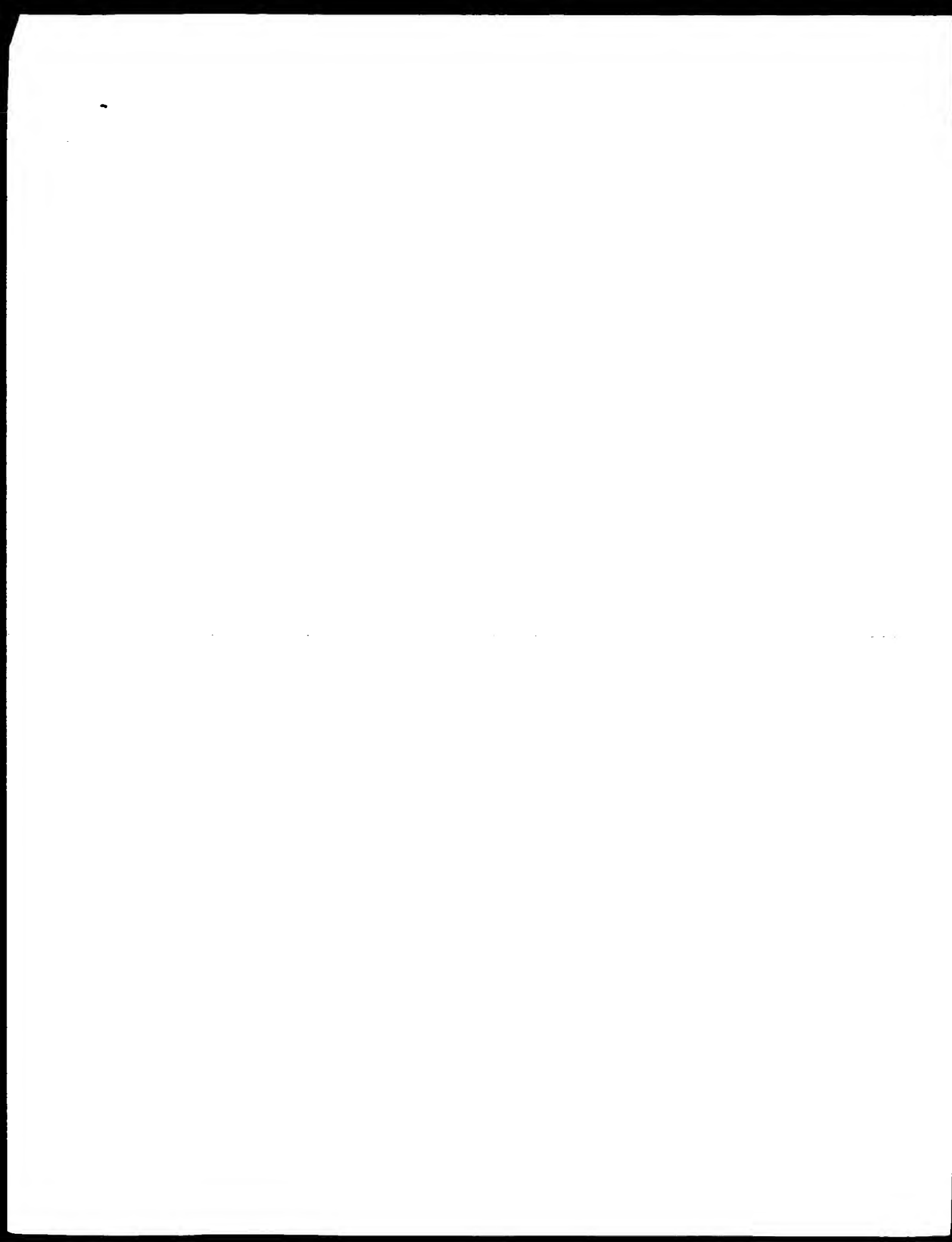
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Page 8



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RESULTS

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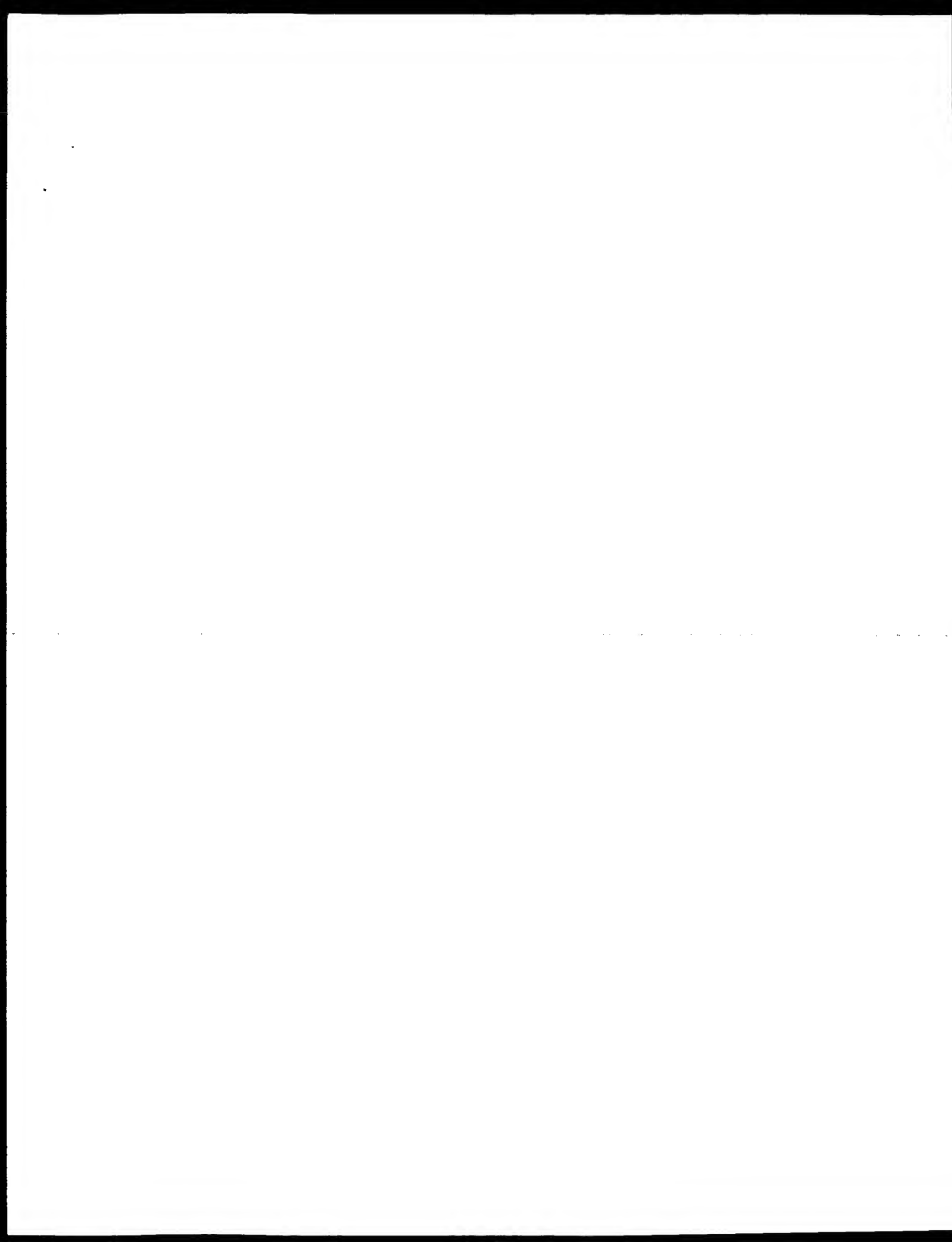
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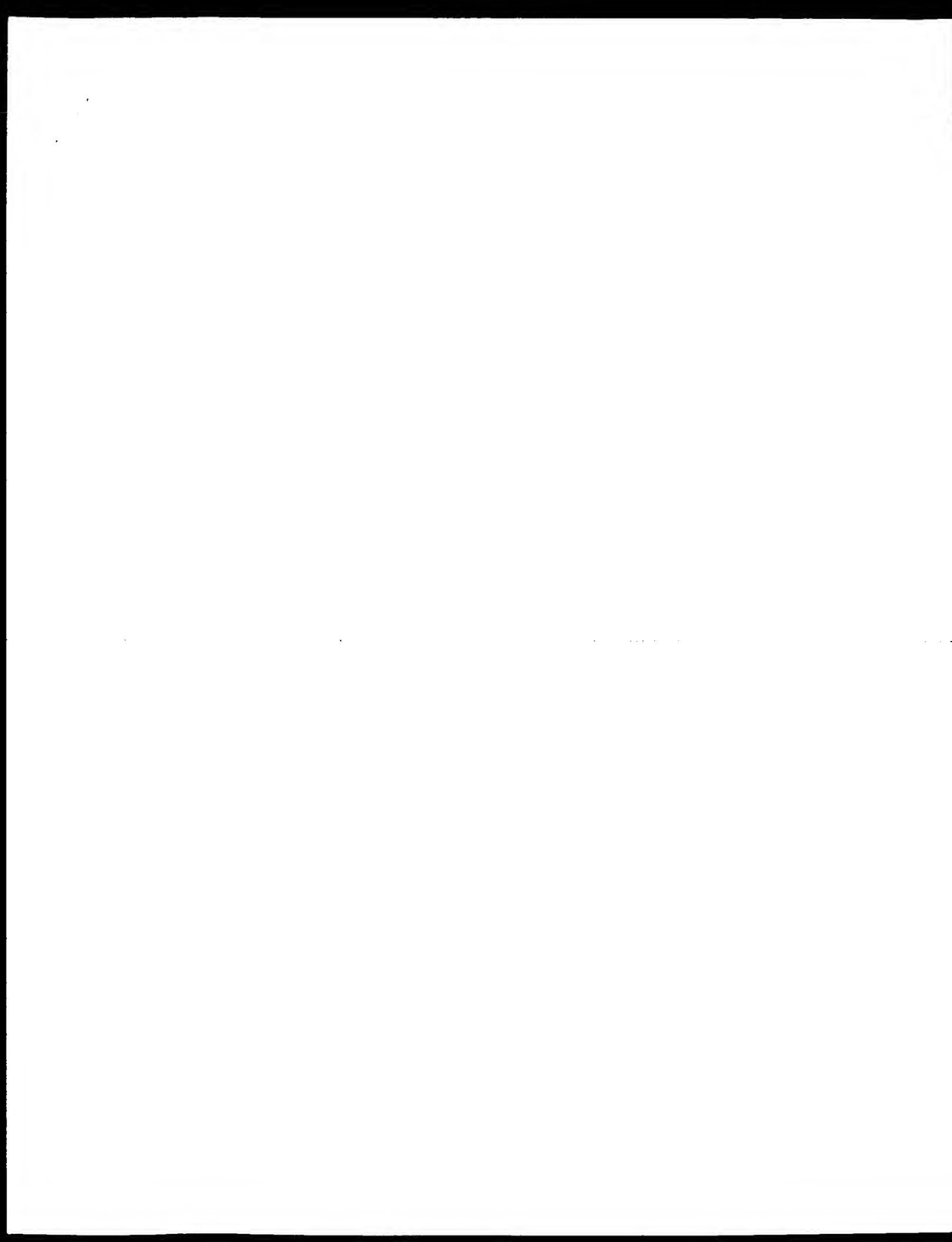
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 DOI: 10.1007/s004070050011
 Printed in the Netherlands

16. HALL, P. J. A. (1980). *Practical Aspects of Protein Sequence Analysis*. London: Chapman & Hall.

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19. HOMO-SOLICÓ (Herman) (1985).



Database: us-09-503-387-16_copy_135_181.rspt
Copyright (c) 1999 - 2000 CompuLink, Inc.

000 proteins - protein search, using SW model

Run on: March 11, 2002, 17:09:16 : Search time: 0.00 seconds
(without database)

91.410 bits/s (approx 0.5)

17.000 proteins - protein search, using SW model

Sequence: 1. US09503387-16-copy_135_181.rspt

Search: 1. US09503387-16-copy_135_181.rspt

Search: 1. US09503387-16-copy_135_181.rspt

Search: 1. US09503387-16-copy_135_181.rspt

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Search: 1. US09503387-16-copy_135_181.rspt

Search: 1. US09503387-16-copy_135_181.rspt

20 87 32.5 1.5 4 0.0016
21 87 32.5 2.0 4 0.0017
22 87 32.5 2.0 4 0.0016
23 87 32.5 2.0 4 0.0016
24 87 32.5 2.0 4 0.0016
25 87 32.5 2.0 4 0.0016
26 87 32.5 2.0 4 0.0016
27 87 32.5 2.0 4 0.0016
28 87 32.5 2.0 4 0.0016
29 87 32.5 2.0 4 0.0016
30 87 32.5 2.0 4 0.0016
31 87 32.5 2.0 4 0.0016
32 87 32.5 2.0 4 0.0016
33 87 32.5 2.0 4 0.0016
34 87 32.5 2.0 4 0.0016
35 87 32.5 2.0 4 0.0016
36 87 32.5 2.0 4 0.0016
37 87 32.5 2.0 4 0.0016
38 87 32.5 2.0 4 0.0016
39 87 32.5 2.0 4 0.0016
40 87 32.5 2.0 4 0.0016
41 87 32.5 2.0 4 0.0016
42 87 32.5 2.0 4 0.0016
43 87 32.5 2.0 4 0.0016
44 87 32.5 2.0 4 0.0016
45 87 32.5 2.0 4 0.0016

AT COMMENTS

Result No. 1
Score: 220
Query: 1. US09503387-16-copy_135_181.rspt

SUMMARY

1 220 82.1 2.1 4 0.0016
2 220 82.1 2.1 4 0.0016
3 220 82.1 2.1 4 0.0016
4 220 82.1 2.1 4 0.0016
5 220 82.1 2.1 4 0.0016
6 220 82.1 2.1 4 0.0016
7 220 82.1 2.1 4 0.0016
8 220 82.1 2.1 4 0.0016
9 220 82.1 2.1 4 0.0016
10 220 82.1 2.1 4 0.0016
11 220 82.1 2.1 4 0.0016
12 220 82.1 2.1 4 0.0016
13 220 82.1 2.1 4 0.0016
14 220 82.1 2.1 4 0.0016
15 220 82.1 2.1 4 0.0016
16 220 82.1 2.1 4 0.0016
17 220 82.1 2.1 4 0.0016
18 220 82.1 2.1 4 0.0016
19 220 82.1 2.1 4 0.0016

20 87 32.5 1.5 4 0.0016
21 87 32.5 2.0 4 0.0017
22 87 32.5 2.0 4 0.0016
23 87 32.5 2.0 4 0.0016
24 87 32.5 2.0 4 0.0016
25 87 32.5 2.0 4 0.0016
26 87 32.5 2.0 4 0.0016
27 87 32.5 2.0 4 0.0016
28 87 32.5 2.0 4 0.0016
29 87 32.5 2.0 4 0.0016
30 87 32.5 2.0 4 0.0016
31 87 32.5 2.0 4 0.0016
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33 87 32.5 2.0 4 0.0016
34 87 32.5 2.0 4 0.0016
35 87 32.5 2.0 4 0.0016
36 87 32.5 2.0 4 0.0016
37 87 32.5 2.0 4 0.0016
38 87 32.5 2.0 4 0.0016
39 87 32.5 2.0 4 0.0016
40 87 32.5 2.0 4 0.0016
41 87 32.5 2.0 4 0.0016
42 87 32.5 2.0 4 0.0016
43 87 32.5 2.0 4 0.0016
44 87 32.5 2.0 4 0.0016
45 87 32.5 2.0 4 0.0016

Mon Mar 11 17:09:16 2002

us-09-503-387-16_copy_135_181.rpt


```

1 FILE REFERENCE: 387-147
2 CURRENT APPLICATION: 09/09/94-468
3 CURRENT FILING DATE: 1999-06-30
4 NUMBER OF SEQUENCES: 24
5 SEQUENCE: 1-24
6 SEQUENCE: 1-24
7 SEQUENCE: 1-24
8 SEQUENCE: 1-24
9 SEQUENCE: 1-24
10 SEQUENCE: 1-24
11 SEQUENCE: 1-24
12 SEQUENCE: 1-24
13 SEQUENCE: 1-24
14 SEQUENCE: 1-24
15 SEQUENCE: 1-24
16 SEQUENCE: 1-24
17 SEQUENCE: 1-24
18 SEQUENCE: 1-24
19 SEQUENCE: 1-24
20 SEQUENCE: 1-24
21 SEQUENCE: 1-24
22 SEQUENCE: 1-24
23 SEQUENCE: 1-24
24 SEQUENCE: 1-24

```

```

Query Match: 82.14% Score: 220.10
Best Local Similarity: 78.76% Prod. No. 6,400,241
Matches: 21 Mismatches: 4

```

```

1 1-24 SEQUENCE: 1-24
2 1-24 SEQUENCE: 1-24
3 1-24 SEQUENCE: 1-24
4 1-24 SEQUENCE: 1-24
5 1-24 SEQUENCE: 1-24
6 1-24 SEQUENCE: 1-24
7 1-24 SEQUENCE: 1-24
8 1-24 SEQUENCE: 1-24
9 1-24 SEQUENCE: 1-24
10 1-24 SEQUENCE: 1-24
11 1-24 SEQUENCE: 1-24
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13 1-24 SEQUENCE: 1-24
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17 1-24 SEQUENCE: 1-24
18 1-24 SEQUENCE: 1-24
19 1-24 SEQUENCE: 1-24
20 1-24 SEQUENCE: 1-24
21 1-24 SEQUENCE: 1-24
22 1-24 SEQUENCE: 1-24
23 1-24 SEQUENCE: 1-24
24 1-24 SEQUENCE: 1-24

```

```

RESULT: 8
US-09-445-408-1
1 Sequence: 1-24
2 Patient No.: 6,400,241
3 GENERAL INFORMATION:
4 APPLICANT: Postfield, S.
5 APPLICANT: Postfield, S.
6 APPLICANT: Postfield, S.
7 APPLICANT: Postfield, S.
8 APPLICANT: Postfield, S.
9 APPLICANT: Postfield, S.
10 APPLICANT: Postfield, S.
11 APPLICANT: Postfield, S.
12 APPLICANT: Postfield, S.
13 APPLICANT: Postfield, S.
14 APPLICANT: Postfield, S.
15 APPLICANT: Postfield, S.
16 APPLICANT: Postfield, S.
17 APPLICANT: Postfield, S.
18 APPLICANT: Postfield, S.
19 APPLICANT: Postfield, S.
20 APPLICANT: Postfield, S.
21 APPLICANT: Postfield, S.
22 APPLICANT: Postfield, S.
23 APPLICANT: Postfield, S.
24 APPLICANT: Postfield, S.

```

```

Query Match: 82.14% Score: 220.10
Best Local Similarity: 78.76% Prod. No. 6,400,241
Matches: 21 Mismatches: 4

```

```

1 1-24 SEQUENCE: 1-24
2 1-24 SEQUENCE: 1-24
3 1-24 SEQUENCE: 1-24
4 1-24 SEQUENCE: 1-24
5 1-24 SEQUENCE: 1-24
6 1-24 SEQUENCE: 1-24
7 1-24 SEQUENCE: 1-24
8 1-24 SEQUENCE: 1-24
9 1-24 SEQUENCE: 1-24
10 1-24 SEQUENCE: 1-24
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15 1-24 SEQUENCE: 1-24
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17 1-24 SEQUENCE: 1-24
18 1-24 SEQUENCE: 1-24
19 1-24 SEQUENCE: 1-24
20 1-24 SEQUENCE: 1-24
21 1-24 SEQUENCE: 1-24
22 1-24 SEQUENCE: 1-24
23 1-24 SEQUENCE: 1-24
24 1-24 SEQUENCE: 1-24

```

```

RESULT: 9
US-09-445-408-12
1 Sequence: 1-24
2 Patient No.: 6,400,241
3 GENERAL INFORMATION:
4 APPLICANT: Postfield, S.
5 APPLICANT: Postfield, S.
6 APPLICANT: Postfield, S.
7 APPLICANT: Postfield, S.
8 APPLICANT: Postfield, S.
9 APPLICANT: Postfield, S.
10 APPLICANT: Postfield, S.
11 APPLICANT: Postfield, S.
12 APPLICANT: Postfield, S.
13 APPLICANT: Postfield, S.
14 APPLICANT: Postfield, S.
15 APPLICANT: Postfield, S.
16 APPLICANT: Postfield, S.
17 APPLICANT: Postfield, S.
18 APPLICANT: Postfield, S.
19 APPLICANT: Postfield, S.
20 APPLICANT: Postfield, S.
21 APPLICANT: Postfield, S.
22 APPLICANT: Postfield, S.
23 APPLICANT: Postfield, S.
24 APPLICANT: Postfield, S.

```

```

Query Match: 43.93% Score: 116.50
Best Local Similarity: 40.00% Prod. No. 6,400,241
Matches: 21 Mismatches: 4

```

```

1 1-24 SEQUENCE: 1-24
2 1-24 SEQUENCE: 1-24
3 1-24 SEQUENCE: 1-24
4 1-24 SEQUENCE: 1-24
5 1-24 SEQUENCE: 1-24
6 1-24 SEQUENCE: 1-24
7 1-24 SEQUENCE: 1-24
8 1-24 SEQUENCE: 1-24
9 1-24 SEQUENCE: 1-24
10 1-24 SEQUENCE: 1-24
11 1-24 SEQUENCE: 1-24
12 1-24 SEQUENCE: 1-24
13 1-24 SEQUENCE: 1-24
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15 1-24 SEQUENCE: 1-24
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17 1-24 SEQUENCE: 1-24
18 1-24 SEQUENCE: 1-24
19 1-24 SEQUENCE: 1-24
20 1-24 SEQUENCE: 1-24
21 1-24 SEQUENCE: 1-24
22 1-24 SEQUENCE: 1-24
23 1-24 SEQUENCE: 1-24
24 1-24 SEQUENCE: 1-24

```

```

RESULT: 10
US-09-989-950-12
1 Sequence: 1-24
2 Patient No.: 6,400,241
3 GENERAL INFORMATION:
4 APPLICANT: Adams, J.
5 APPLICANT: Adams, J.
6 APPLICANT: Adams, J.
7 APPLICANT: Adams, J.
8 APPLICANT: Adams, J.
9 APPLICANT: Adams, J.
10 APPLICANT: Adams, J.
11 APPLICANT: Adams, J.
12 APPLICANT: Adams, J.
13 APPLICANT: Adams, J.
14 APPLICANT: Adams, J.
15 APPLICANT: Adams, J.
16 APPLICANT: Adams, J.
17 APPLICANT: Adams, J.
18 APPLICANT: Adams, J.
19 APPLICANT: Adams, J.
20 APPLICANT: Adams, J.
21 APPLICANT: Adams, J.
22 APPLICANT: Adams, J.
23 APPLICANT: Adams, J.
24 APPLICANT: Adams, J.

```

```

Query Match: 43.93% Score: 116.50
Best Local Similarity: 40.00% Prod. No. 6,400,241
Matches: 21 Mismatches: 4

```

```

1 1-24 SEQUENCE: 1-24
2 1-24 SEQUENCE: 1-24
3 1-24 SEQUENCE: 1-24
4 1-24 SEQUENCE: 1-24
5 1-24 SEQUENCE: 1-24
6 1-24 SEQUENCE: 1-24
7 1-24 SEQUENCE: 1-24
8 1-24 SEQUENCE: 1-24
9 1-24 SEQUENCE: 1-24
10 1-24 SEQUENCE: 1-24
11 1-24 SEQUENCE: 1-24
12 1-24 SEQUENCE: 1-24
13 1-24 SEQUENCE: 1-24
14 1-24 SEQUENCE: 1-24
15 1-24 SEQUENCE: 1-24
16 1-24 SEQUENCE: 1-24
17 1-24 SEQUENCE: 1-24
18 1-24 SEQUENCE: 1-24
19 1-24 SEQUENCE: 1-24
20 1-24 SEQUENCE: 1-24
21 1-24 SEQUENCE: 1-24
22 1-24 SEQUENCE: 1-24
23 1-24 SEQUENCE: 1-24
24 1-24 SEQUENCE: 1-24

```

```

RESULT: 11
US-09-989-950-16
1 Sequence: 1-24
2 Patient No.: 6,400,241
3 GENERAL INFORMATION:
4 APPLICANT: Adams, J.
5 APPLICANT: Adams, J.
6 APPLICANT: Adams, J.
7 APPLICANT: Adams, J.
8 APPLICANT: Adams, J.
9 APPLICANT: Adams, J.
10 APPLICANT: Adams, J.
11 APPLICANT: Adams, J.
12 APPLICANT: Adams, J.
13 APPLICANT: Adams, J.
14 APPLICANT: Adams, J.
15 APPLICANT: Adams, J.
16 APPLICANT: Adams, J.
17 APPLICANT: Adams, J.
18 APPLICANT: Adams, J.
19 APPLICANT: Adams, J.
20 APPLICANT: Adams, J.
21 APPLICANT: Adams, J.
22 APPLICANT: Adams, J.
23 APPLICANT: Adams, J.
24 APPLICANT: Adams, J.

```


Genotype version: 1.5
Copyright (c) 1997 - 2000, Nephosys Inc.

Run on: March 11, 2002, 16:46:07 / Search: 1000 / Size of results: 245,709 hits / 1000 / 414,075

Filter: 1000
Filter score: 1000
Sequence: 1000
Search: 1000

Search: 21921 seqs, 7617452 residues

Total number of hits satisfying chosen parameters: 21921

Minimum job seq length: 10
Maximum job seq length: 20000000

Post-processing: Minimum Match: 100
Maximum Match: 1000
Filtering filter: 45 Summaries

Database: 1: EMBL
2: F111
3: F112
4: F113
5: F114

Prod. No. is the number of results returned by the search engine. The score given is the score of the top hit. The score of the top hit is the score of the top hit and is derived by analysis of the top hit sequence.

Summary

Result No.	Score	Query	Match	Length	DB	ID
1	876.5	67.3	264	2	146020	
2	876.5	29.3	641	2	105884	
3	876.5	29.3	641	2	105884	
4	869.5	27.7	635	2	105884	
5	849.5	26.7	635	2	105884	
6	849.5	26.7	635	2	105884	
7	841.5	26.0	296	2	105884	
8	834	25.5	135	2	105884	
9	819	24.1	193	2	105884	
10	816	24.1	239	2	105884	
11	810.5	23.7	444	2	105884	
12	810	23.7	287	2	105884	
13	806.5	23.4	444	2	105884	
14	806.5	23.4	444	2	105884	
15	802.5	22.3	146	2	105884	
16	802.5	22.3	146	2	105884	
17	802.5	22.3	146	2	105884	
18	802.5	22.3	146	2	105884	
19	802.5	22.3	146	2	105884	
20	802.5	22.3	146	2	105884	
21	802.5	22.3	146	2	105884	
22	802.5	22.3	146	2	105884	
23	802.5	22.3	146	2	105884	
24	802.5	22.3	146	2	105884	
25	802.5	22.3	146	2	105884	
26	802.5	22.3	146	2	105884	
27	802.5	22.3	146	2	105884	
28	802.5	22.3	146	2	105884	
29	802.5	22.3	146	2	105884	
30	802.5	22.3	146	2	105884	

Alignments

1	876.5	67.3	264	2	146020	
2	876.5	29.3	641	2	105884	
3	876.5	29.3	641	2	105884	
4	869.5	27.7	635	2	105884	
5	849.5	26.7	635	2	105884	
6	849.5	26.7	635	2	105884	
7	841.5	26.0	296	2	105884	
8	834	25.5	135	2	105884	
9	819	24.1	193	2	105884	
10	816	24.1	239	2	105884	
11	810.5	23.7	444	2	105884	
12	810	23.7	287	2	105884	
13	806.5	23.4	444	2	105884	
14	806.5	23.4	444	2	105884	
15	802.5	22.3	146	2	105884	
16	802.5	22.3	146	2	105884	
17	802.5	22.3	146	2	105884	
18	802.5	22.3	146	2	105884	
19	802.5	22.3	146	2	105884	
20	802.5	22.3	146	2	105884	
21	802.5	22.3	146	2	105884	
22	802.5	22.3	146	2	105884	
23	802.5	22.3	146	2	105884	
24	802.5	22.3	146	2	105884	
25	802.5	22.3	146	2	105884	
26	802.5	22.3	146	2	105884	
27	802.5	22.3	146	2	105884	
28	802.5	22.3	146	2	105884	
29	802.5	22.3	146	2	105884	
30	802.5	22.3	146	2	105884	

[illegible]

THE UNIVERSITY OF CHICAGO PRESS

[illegible]

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85															

[illegible]



GenBank version 4.5
Copyright (c) 1993-2000 Computer 1.0.1

cd protein protein search, using sw model

from: March 11, 2002, 17:09:22, 16 copy_22_267.rspc

GenBank version 4.5
Copyright (c) 1993-2000 Computer 1.0.1

111101
Perfect score: 0.8
Sequence: 1 US09503-387-16_COPY_22_267

Search: 1 US09503-387-16_COPY_22_267

Gapop: 10.0, Gapext: 0.5

Seatched: 473505 seqs, 14522229 seqs, 14522229

Total number of hits satisfying chosen parameters: 473505

Maximum hit seq length: 6

Maximum hit seq length: 200000000

Post-Processing: Maximum Match: 0.8

Maximum Match: 100%

Database: 1: SP_000001_17*

2: SP_000002*

3: SP_000003*

4: SP_000004*

5: SP_000005*

6: SP_000006*

7: SP_000007*

8: SP_000008*

9: SP_000009*

10: SP_000010*

11: SP_000011*

12: SP_000012*

13: SP_000013*

14: SP_000014*

Prod. No. is the number of results produced by the search. The score is the score of the best hit. The score is the score of the best hit. The score is the score of the best hit.

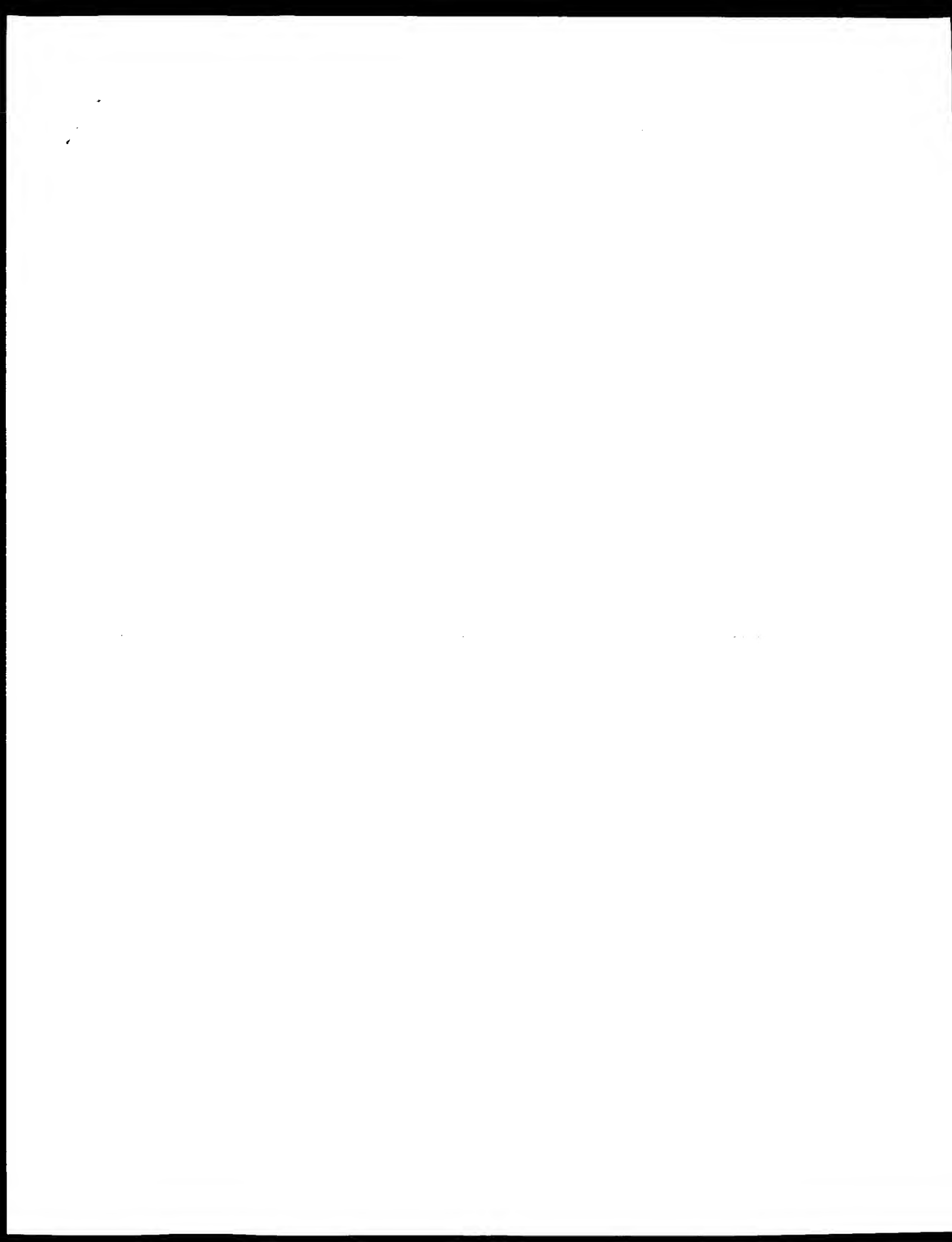
SUMMARIES

Result No.	Score	Match	Length	Hit
1	805.5	62.4	439	4 US09503-387-16_COPY_22_267
2	804.5	62.0	439	4 US09503-387-16_COPY_22_267
3	817.5	61.1	421	1 US09503-387-16_COPY_22_267
4	437.5	33.5	448	1 US09503-387-16_COPY_22_267
5	437.5	33.5	448	1 US09503-387-16_COPY_22_267
6	437.5	33.5	448	1 US09503-387-16_COPY_22_267
7	437.5	33.5	448	1 US09503-387-16_COPY_22_267
8	437.5	33.5	448	1 US09503-387-16_COPY_22_267
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21	437.5	27.4	429	4 US09503-387-16_COPY_22_267
22	437.5	26.7	429	4 US09503-387-16_COPY_22_267
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44	437.5	26.4	429	4 US09503-387-16_COPY_22_267
45	437.5	26.4	429	4 US09503-387-16_COPY_22_267

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1	US09503-387-16_COPY_22_267
2	US09503-387-16_COPY_22_267
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1 TITLE OF INVENTION: GYDROLYZED VI AND USIN THEREOF
 2 FILE REFERENCE: 79/071514
 3 CURRENT FILING DATE: 1999/06/22
 4 NUMBER OF SEQ. ID NOS: 24
 5 SUMMARY: FURTHER INFORMATION WITHIN
 6 SEQ. ID NO. 5
 7 LENGTH: 419
 8 TYPE: PRT
 9 ORGANISM: Homo sapiens
 10 US-09-345-408-5

Query Match: 69.4%, Score 905.5, ID: 4, Length: 419
 Best Local Similarity: 69.4%, Prod. No: 6,645,408
 Matches: 174, Conserved: 18, Mismatches: 54, Indels: 0
 1 GENE: GYDROLYZED VI AND USIN THEREOF
 2 FILE REFERENCE: 79/071514
 3 CURRENT FILING DATE: 1999/06/22
 4 NUMBER OF SEQ. ID NOS: 24
 5 SUMMARY: FURTHER INFORMATION WITHIN
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 9 ORGANISM: Homo sapiens
 10 US-09-345-408-5
 11 GENE: GYDROLYZED VI AND USIN THEREOF
 12 FILE REFERENCE: 79/071514
 13 CURRENT FILING DATE: 1999/06/22
 14 NUMBER OF SEQ. ID NOS: 24
 15 SUMMARY: FURTHER INFORMATION WITHIN
 16 SEQ. ID NO. 5
 17 LENGTH: 419
 18 TYPE: PRT
 19 ORGANISM: Homo sapiens
 20 US-09-345-408-5

RESULT: 6
 US-09-345-408-4
 1 GENE: GYDROLYZED VI AND USIN THEREOF
 2 FILE REFERENCE: 79/071514
 3 CURRENT FILING DATE: 1999/06/22
 4 NUMBER OF SEQ. ID NOS: 24
 5 SUMMARY: FURTHER INFORMATION WITHIN
 6 SEQ. ID NO. 5
 7 LENGTH: 419
 8 TYPE: PRT
 9 ORGANISM: Homo sapiens
 10 US-09-345-408-4

Query Match: 69.4%, Score 905.5, ID: 4, Length: 419
 Best Local Similarity: 69.4%, Prod. No: 6,645,408
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RESULT: 6
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RESOLUTION 12
05-08-965,950-18

Suspense 18; Application 05/08965,950

Patent No. 6,140,076

GENERAL INFORMATION:

APPLICANT: Adolfo Dasso, Inc.

TITLE OF INVENTION: Isolated Mammalian Monoclonal Cell Lines

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ORGANIZATION: Fred Posner's Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

MOLECULAR RELEVANCE TERM:

MEDIUM TYPE: Polypeptide

COMMENTS: Immune response

FEEDBACK SYSTEM: In-house

SEQUENCE: Exposed to nucleic acid

CURRENT APPLICATION NO.: 6,140,076

DATE OF RECEIPT: 05/08965,950

FILING DATE: 05-15-1997

CLASSIFICATION: A20

REMARKS: This application was filed as a continuation-in-part of U.S. Patent No. 6,140,076.

